```
Conform vorsion 5 1,3 Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

January 16, 2003, 16:39:12 - Seatch time 7-28*71 Seconds (without alignments) 28-464 Million cell updates/sec Run on:

US-09-856-070-26 28 1 QDYEE 5 Title: Perfect score: Sequence:

Scoring table:

112892 scqs, 41476328 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing lirst 45 summaries

SwissProt_40:* Database : Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by adalysis of the total score distribution

SUMMARIES

Description	Q9y506 homo sapien	9 7 1 1	O14832 homo sapien	_		P31976 Fis Laurus		Q39493 cylindrothe	m		_	3 home		099mp3 mus muscula	P10093 rattus morv	_	203683 niroliana :	_	P95019 myccharter;	ت	P44464 hacmophilus	-	- 1	057678 methanococc	F42280 drusophila	C9p7c6 schizosacch	Q03681 nicotiana t	Q03682 nicetiana t	Q03686 micretiana 1	P20774 homo sapies	bos t		たが見られて現在との例 というといん
ID	ė,	ORC6_MOUSE	PAHX_HUMAN	SYW_PYRAB	SYE_CHLPN	FERT_BOVIN	EZRI_HUMAN	DSK1_CYLFU	Odnja OAS	DD20_HUMAN	PESO MOUSE	I KAF_HUMAN	Y070_METJA	CAL2_MOUSE	CALL RAT	VG36_HAEIN	BIF3_TOBAC	EFP_MYCLE	EFP_MYCTU	LOCC_DROME	LIPB_HABIN	THESTANETH	IF31_HUMAN	Y225_METJA	TFY?_DF WE	CWFN_SCHPO	BIP1_TOBAC	RIP2_TORAC	RIP8_TOBAC	OIF_HITMAN	OIF_BOVIN	YC4W_1EAS1	YCCJ_YFAST
ad	-	_		-			- 4	_	-1	-	٠.	-4	_	-	- -	,	-1	_	1	٠.		٠.	-1		٠,	,- -		-	provide the	٠.	-	_	-
Length	25.	202	338	385	505	C.R.C.	(၂) (၂)	624	i Lo	824	80.1	1332	8.7	130	3.34	141	168	187	187	203	C1	533	558 518	263	CBC	583	290	7.5°C	293	298	546	315	339
% Ouery Match	190 0	100.0	100.0	100.0	100.0	100 0	100.0	100.0	100 n	100.0	100 0	100.0	89.3	89.3	89.3	\circ	89.3	89.3	ट ठ	Ö	89.3	89.3	89.3	89.3	ح ح 80	89.3	89.3	83 3	80.2	80 8		83.3	~ ق
Score	œ.c.	8.7	28	28	28	28	28	58	28	28	œ. □	87	25	25	25	25	និ	25	25	C1	10 10 10 10 10 10 10 10 10 10 10 10 10 1	55	(1) 근1	52	un Cil	r.	25	C.I	un Cit	25	25	un Cil	55
Result No.		(4	3	4	S	9	7	œ	6	10	11	12	13	14	15	16	17	18	5.1	50	21	근	೯೭	77.	ET C 1	92	27	යා උ1	ڻ د د	30	31	3.2	33

		######################################					PGL2_ASPNO PGL2_ASPNO REQ2_XENLA REQ2_XENLA REQ0_HUMAN REQ0_HUMAN REQ0_HUMAN REQ0_CRGE REQ0_CRGE REQ0_CRGE REQ0_CRGE OFFICE ASPNO REQ0_CRGE REQ0_C	NC LIA LIA LIA LIA LIA LIA LIA LIA LIA LIA	P25214 P19805 QQW6336 QQW7838 Q62710 Q611113 Q611113 Q611103 Q611103 Q611103 Q611103	aspe aspe xeno xeno homo homo homo cory qall sace salm	aspergillus xenopus lae xenopus lae xenopus lae homo sapien mus musculu synechocyst volynebacto qallus qall satechi.cayv salmonella	
							ALIGNMENT	MENTS				
	to to	RESULT 1 ORC6_HUMAN ID ORC6_HUMA	z	STAN	ARD;		PRT;	252 AA.				
- -	AC DI DE	O9Y5N6. 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last seque 16-OCT-2001 (Rel. 40, Last annot Origin recognition complex subun	001 (001 (001 (Rel. 4(Rel. 4(Rel. 4(Rel. 4(0, Cre 0, Las 0, Las comple	ate t s x	ed) equence unnotatic ubunit 6	ed) sequence update) annotation update) subunit 6.				
		ORCEL. Homo sapiens (Human Eukaryota; Metazoa Mammalia; Eutheria NCHI_TaxIU=9606;	ens Fime Eut D≡96	(Human). etazoa: Chordata: Lheria: Primates: 606;). Chord Prima	lata	; Calari	Graniata; Vertebrata; Eutele Catarrhini; Hominidae; Homo.	; Euteleostomi e; Homo.	tomi;		
		11] SEQUENCE FROM N.A. Dean F.B., O'Donnell M.; "-PRA "1 offs; of a bresied for Sa	FROP , o' in Ling	N.A. Donnell	M T	÷	Por Salvifi	atjsjaatea seakwatapa es	٠٠ <u>ق</u>	mo:	1.cm Homo	
· · · · · · · · · · · · · · · · · · ·	# # 0 0 0 0 0 1 d	sapiens." Submitted -!- FUNCT BINDS REPLI	CATI	COMPORTING OF AND AND AND CONSENSE	NENT OF THE NENT OF MATIN	he PFT ICA IG I	FMBL /Gee THE ORIGI ATION. IT YPE TRAN	Sublens." Submitted (MAP-1949) to the FMBL/Genbank/Innul databases. -i- FUNCTION COMPONENT OF THE CREATEN RECOGNITION COMPLEX (CHC) THAT BINDS ORIGINS OF REPLICATION. IT HAS A FOLE IN HOTH CHOOMOSOMAL REPLICATION AND MATHOR TRANSFEPTIONAL SILENCING. BINDS TO THE APS CONSENSUS SEQUENCE (APS) OF OPIGINS OF REPLICATION IN AN	bases. COMPLEX (OU BOTH CHRO? LENCING, B. REPLICATIO	RC) T MOSOM INDS ON IN	HAT AL TO AN	
:	3288	ALF-I -1- SUBCE -1- SUBCE -1- SIMIL	LIT:	CENT MI CEC 1S AR LOCA Y: BELA	ANNEK.	SEL Nu	OF SIX ICLEAT. HE ORC6	SUBUNITS. FAMILY.				
	85888858	This swift between the burop ase by modified entities of send a	the round requirements	Swiss Swiss Bioinfo profit this st	i) is Instit Ormati inst inst Lateme Licen	cs cs interest sea	yright. For Bioi Institut trions as is not a	This SWISS PPOT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBs outstation the European Bioinformatics institute. There are no restrictions on its asc by non-profit institutions as long as its content is in no way modified and this statement is not removed. Saage by and for commercial entities requires a litter and the profit is a commercial or send an email to license@isb-sib.ch).	thicold a the EMBS of the EMBS	Lout Lout Ction ction s in for c	ahorati station s on h no s	ion its its iai
	N M D R	EMBL, AFI Genew, HC DNA repli SECCENCE	3965 386.1 387.1	58; AAD 7151; (OIL; Nuc	32666. ORC66. clear 28106	1 T. T.		EMBL) AF139658; AAD32666.1; Genew, HGNC.17151; ORG60. DNA replication; Nuclear protein; DNA-binding. SECENCE LCLAA, 28196 MW, 78840387695145FE CEC64;	064,	1 1 1		
	Bes Matt	ry Matel t Local ches	Time 3	similarity 5, Conserve	190.0%; 190.0%; Vative 0	* 60	ώ. <u>→</u>	28, DB 1, Le No. 35; atches 0;	Length 252; Indels (0; 6	Gaps	0;
	O	1 QDYEE 	ro ⊂1	34								
	HESULT OPCS_M ID O AC Q UI I	PERSULT 2 OPCG_MOUSE ID OPCG_MOUSE AC Q9WUJ8; EI 16 OCI-2001		STANDARD: (Rel. 40, Created)	STANDARD:	ia to	PPT;	262 AA.				
_	Ţ	16 - 20T - 20		. F. S. 4.	S, 1.45	<i>n</i>	(agripdin asymptos)	update)				

```
This SWISS-PROF entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Biointormatics and the EMBL outstation the European Biointormatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb.sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                    Dean F.B., O'Donnell M.; "CDNA Cloning of a homolog for Saccharomyces cerevisiae ORC6 from Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THE ARS CONSENSUS SEGREBLE (ACS) OF OPIGINS OF PERLICATION IN AN ATP DEPENDENT MANNER (BY SIMILARITY).
SURMINT: OR 'IS COMPOSED OF SIX SIMILARITY)
SURMINT: OR 'IS COMPOSED (By SIMILARITY)
SUBCELLULAR EXCATION: Nuclear (By Similarity).
SIMILARITY: HELONGS TO THE ORCG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-1999) to the EMBL/GHORALYDERI databases -!- FUNCTION: COMPONENT OF THE ORIGIN RECOGNITION COMPLEX (ORC) THAT BINDS ORIGINS OF REPLICATION. II HAS A FOLE IN BOTH CHROMOSOMAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPLICATION AND MATING TYPE TRANSCRIPTIONAL SILENCING, BINDS TO
                                                                                                   Mus musculus (Mouse).
Enkaryota: Mctazoa; Chordsta; Craniata; Vertebrsta; Esteleostomi;
Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mihalik S.J., Morrell J.C., Kim D., Sachsteder K.A., Watkins P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jansen G.A., Ofman R. Ferdinandusse S., Ijist I., Muijsers A.O., Skjeldal O.H., Stokke O., Jakobs G., Besley G.I.N., Wraith J.E., Wanders R.J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Cherdata: Crantata; Vertebrata; Eutelocetomi;
Mammalta; Butheria; Primates; Catarrbini; Heminidae, Bone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1999 (Rel. 8), created)
15-JUL-1999 (Rel. 8), last sequence update)
15-JUN-2002 (Rel. 4), last annotation update)
15-JUN-2004 dioxygenasc, peroxisomel procursor (PC 1-14-11.18)
19474anoyl-CoA dioxygenasc, peroxisomel procursor (PC 1-14-11.18)
(Phytanoyl-CoA alpha-hydroxylasc) (Phytanoyl-CoA alpha-hydroxylasc) (Phytanoyl-CoA alpha-hydroxylasc)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "ketsum disease is caused by mutations in the phytanoyl-CoA hydroxylase gene.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 28; DB 1; Length 262; 100.0%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA replication; Nuclear protein; DNA-binding,
SEQUENCE 262 AA; 29188 MW; F8027HF9C87HH16C CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification of PAHX, a Refsum disease gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND VAPIANT PEFSHM TPP-275.
MEDLINE-97467730; PubMed-9326939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND VAPIANT REFSHM HIS-269
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.38 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                   origin recognition complex subunit 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97467731; PubMed-9426940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nat. Genet. 17:185-189(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF139659; AAD32667.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD: MGI:1929285; orc61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
Hes 5, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUTENCE FROM N A
                                                                                                                                                                                                                                                                           SHOUENCE FROM N.A.
                                                                                                                                                                                                           NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCB1_TaxTD=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 CDYEE 244
                                                                          ORCEL OR ORCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ODYEE 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHYH OR PAHX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAHX HUMAN
                                                                                                                                                                                                                                                                                                                                                                           musculus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Could S.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           014832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARX_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESHLT *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and to commercial entities requires a license agreement (See http://www.isb.sib.ch/announce.) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                           Jansen G.A., Hogenhout E.M., Fordinandusse S., Waterham H.K., Ofman R., Jakobs C., Skjeldal O.H., Wanders R.J.A.; Furtinandus P. J., Wanders R.J.A.; Human phytancyl CoA hydroxylase. resolution of the gene structure and the molecular basis of Relaun's disease."; Hum. Mcl. Genet. 9:1195-1200(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABNORMALITIES, ICHIHYOSIS, CATARACTS AND CARDIAC IMPAIRMENT.
MANIFESTATIONS OF THE DISEASE APPEAR IN THE SECOND OR THIRD DECADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECTFICTTY: EXPRESSED IN LIVER, KIDNEY, AND T-FELLS, HUT NOT IN SPILEN, BRAIN, HEART, LUNG, AND SKELEIAL MUSCLE.
DISEASE: DEPECTS IN PHYL ARE THE CAUSE OF REPSUM DISEASE; AN AUTOSWAL RECESSIVE DISROBER CHARACTERIZED CLINICALLY BY A TETRAD OF ABNORMALITIES: RETINITIS PIGMENTOSA, PERIPHERAL MEDIOPATHY, CEREBELLAR ATAXIA, AND ELEVATED PROTEIN LEVELS IN THE
                                                                                                           Baulieu E.-E.; "Immunophilins, refsum disease, and lupus nephritis: the peroxisomal
                                                                     MEDLINE-99162565; FutMed-10051602;
Chambraud B., Radanyi C., Camonis J.H., Rajkowski K., Schumacher M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CEREMEGSPINAL FLUID (CSF), PATIENTS EXHIBIT ACCOMULATION OF THE BRANCHED-CHAIN FATTY ACID, PHYLANIC ACID, IN BLOOD AND IISSUES. LESS CONSTANT FEATURES ARE NERVE DEAFNESS, ANOSMIA, SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        > W (IN REPSOM; LOSS OF ACTIVITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (phytanic acid); serond step.
-!* SUBUNI: INTERACTS SPECIFICALLY WITH THE IMMUNOPHILIN FKRP52.
                                                                                                                                                   enzyme_phytancyl-COA alpha-hydroxylase is a new FKBP-associated
                                                                                                                                                                                                                                                                                                                                           Hum. Mcl. Genet. 9:1155-1200(2000).
FUNCTION: CONVEPTS PHYTANGYL-COA TO 2-HYDROXYPHYTANGYL-COA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PATHWAY: Alpha-oxidation of 3-methyl branched fatty acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase, Peroxisome, Vitamin C, Iron, Thansit peptide,
                                                                                                                                                                                                                                                                                                                                                                                    2-oxoglutarate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MICROBODY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHYTANOYL-COA DIOXYGENASE
                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND VARIANT REFSUR ALA-192 INS
                                                                                                                                                                                       Proc. Natl. Agad. Sci. U.S.A. 96:2104-2109(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A -> AA (IN REFSUM).
/FIId-VAR_012980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R : H (IN REFSOM).
/FTId-VAR_005525.
                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: Phytanoyl-CoA \sim 2 - 6 \times 6 hydroxyphytanoyl-CoA \leftrightarrow 8 \text{uccinate} \leftrightarrow CO(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId-VAR 005526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Peroxisomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AT112977; AAD20602.1; -.
EMBL, AP242349; AAF74123.1; -.
EMBL, AF242379; AAF74123.1; -.
EMBL, AF242380; AAF74123.1; JOINED.
EMBL, AF242381; AAF74123.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF242383, AAF74123.1; JOINED.
AF242384; AAF74123.1; JOINED.
AF242385; AAF74123.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                    -!- COFACIOR: Iron and ascorbate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38538 MW;
Nat. Genet. 17:190-193(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF023462; AAB81834.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC:8940; PHYH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338 AA;
                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disease mutation.
                                                       TISSUE-Leukemia;
                                                                                                                                                                                                                                                 PubMed-10767344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            602026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OF LIFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANS 1 T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAPIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM
```

FBF9639E7C79A6B0 CRC64;

```
BINDING
                                                                    (Gluks)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP;
   PUBLICA CONTRACT TO THE CONTRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a lineuse agreement (see http://www.isb.sib.cn/announce/or send an email to licensewisb-sib.ch).
                                                                                                   زز
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Pyrococcus abyssi denome sequence, insights into archaeal chromosome structure and evolution.";
structure and evolution.";
Submitted (JUL-1999) to the EMRL/GenRank/PDRT databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Aminoacyl:tRNA synthetase, Protein blosynthesis; Ligase; AIP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea, Euryarchaebta, Phermococci, Thermococcales, Thermotochaebae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: AIP + L-'Irypiophan + LPNA(Trp) - AMP + diphosphate + L-tryptcphanyl-tkNA(Trp). -!- SUBCELLULAR LOCATION: Cytoplasmic. -: SUBCELLULAR LOCATION: Cytoplasmic. -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan +tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ċ
                                                                                               0
                              100.0%; Score 28, DB 1; Length 338; 100.0%; Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 28; DB 1; Length 385; 100.0%; Pred. No. 56;
                                                                                               9, indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4029N01414976R12 CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "HIGH" REGION.
"KMSKS" REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYE_CHLDN STANDARD, PPT, 505 AA, 092723; 094014; 30-MAY-2000 (Pel 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update)
                                                                                            0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AJ248288; CAH50601.1; ...
InterPro; IPR002305; TPP_EMRA synt_lb.
InterPro; IPR002305; TEMA synt_lb.
IDTOFPRO; IPR001412; LRMA synt_lb.
                                                                                                                                                                                                                                                                                                                                                                                                                       090<u>Y</u>11;
15-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIAM: PF00579; LRNA-SYNL 1b; 1
PRINTS: PR01039; TRNASYNTHIRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     385 AA; 45100 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T1GR00233; trps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.0
nes 5; Conservative
Query Match
Rest Local Similarity 100,
The 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-GE5 / Orsay:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRPS OR PABILLI.
                                                                                                                                                                                                                       237 QDYEE 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 QDYEE 70
                                                                                                                                                             1 ODYEE 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ODYPER 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heilig R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                            SYW_PYRAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIGREAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYE_CHLPN
                                                                                                                                                                                                                                                                                                                                                             SYW_PYRAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                               NO CONTRACTOR OF THE CONTRACT OF THE CONTRACT
```

```
This SWISS-FROT entry is copyright, It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial edities tequires a license afterement (see http://www.isb a.b.ch/announce or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback L., Herry K., Bass S., Linher K., Weidman J., Khourl H., Graven B., Bowman C., Bodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tRNA synthetase: Protein biosynthesis, Ligase; ALP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- SUBUNI: MONOMER (HY SIMILARITY).
-:- SUBCELLULAR LOCATION CYPOPLASMIC.
-:- SIMILARITY: BELONGS TO CLASS-! AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE 20330349; PutMed 10871362; Minclo M., Tabuchi M., Kishi F., Cuchi K., Shiral M., Hirakawa H., Kimolo M., Tabuchi M., Kishi F., Cuchi K., Shiba T., Ishi K., Hattori M., Kuhara S., Nakazawa T.; Comparison of Whole genome sequences of Chlamydia preumoniae J138 from Japan and CWL029 from USA.".

Nucleic Acids Res. 28:2311-2314(2096).

--- "ALANYTI" ALF L-qiutamyl-tRNA(Glu).
                                                                                                                                                                                                                                                                                                                                                          Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Ollnyer L., Grimwood J., Davis R.W., Stephens R.S., "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
                                  Glatamyl-tPNA syntherase (EC 6.1.1.17) (Glutamate--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 28; DB 1; Length 505; 100.0%; Pred. No. 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "KMSKS" REGION.
ATP (BY SIMILARITY).
91B580D7C31E6695 CRC64;
                                                                                                                             Chiamydia pneumoniae (Chiamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
16-00T-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "HIGH" REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae AR39.";
Nucleic Acids Ros 28-1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IFR034527, 01tX_bact.
|PR0309245 Glu_tRNA-synt_lc.
|PR001412; tRNA-synt_l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam: PFG0745; LRNA-Synt_lc; 1.
PRINTS, PRG0287; TRNASYNHHGLU.
TIGFRAMS, TIGR09464; qltx bact; 1.
PROSITE; PSG0178; AA_TRNA_LIGASE_I; 1.
                                                                                                                                                                                                                                                                                                                            MEDLINE-99205606; Pubmed-10192388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20150255; PubMed-10684935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL: AFOOTEAD: AASTR700,1; -,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AR002180; AAF38063.1; -. AP002547; BAA98766.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58205 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nut. Cenet. 21:385-389(1999).
                                                                                                  31.1X OR CPN0560 OR Cr0190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Hest Local Similarity Tuo.x
5. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            505 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P27000; 1GLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
                                                                                                                                                                                                                                                                                                 SIRAIN-CWL029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGR; CP0190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STEATN-AR39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aminoacy] .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterFro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
```

o,

us-09-856-070-26.rsp

351 QDYER 355

```
RESULT 7
                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation—the European Hobinformatics institute. There are no restrictions on its use by non-prolit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or soud an email to license above.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Galat A., Gerbod M.C., Bonet F., Riviere S., "Proteins and their amino acid compositions: uniqueness, variability,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arch. Biochem. Biophys. 330:229-237(1996).
-1- FUNCTION: PROHABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL STRUCTURES TO THE PLASMA MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bergson C.M., Zhao H., Saijoh K., Duman R.S., Nestler E.J.; Ferrin and Osttoonettin, two proteins associated with cell shape and growth, are enriched in the locus cocruleus."; Mol. Cell. Neurosci. 4:64-73(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Sraniata, Vertebrata, Euteleostomi,
Mammalia: Eutheria, Cetartiodactyla; Ruminantia; Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 SUBCELLULAR LOCATION: MICROVILLAR PERIPHERAL MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHORYLATION (BY PDGFR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION (BY PDGFR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ECD663E5C200FAA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CYTOPLASMIC SIDE).
-1- PTM: PHOSPHORYLATED BY PROTEIN-TYROSINF KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00660; BAND_41_1; 1.
PROSITE; PS00661; BAND_41_2; 1.
PROSITE; PS0057; BAND_41_2; 1.
Structural protein; Cytoskeleton; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    !- SIMILARITY: CONTAINS | BAND 4.1-LIKE DOMAIN.
                                                                                                                                                                                                                                                               01.30L.1993 (Rel. 26, Created)
01.30L.1993 (Rel. 26, Last sequence update)
16.0CF-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARILY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 28; DB 100.0%; Pred. No. 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAND 4.1-LIKE.
                                                                                                                                                                                                                                                                                                                                                                    Ezrin (p81) (Cytovillin) (Villin 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR000798; Ez/rad/moesin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIŠSUE-Kidney;
MEDLINE-96239137; PubMed-8660651;
Galat A., Gerbod M.C., Bonet F., R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000299; Blod_4.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                580 AA; 68629 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-15 AND 126-140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M98498; AAA30510.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfan, FF60373, Band 41: 1
                                                                                                                                                                                                                STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS: PR00935; BAND41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM00295; B41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boyldae; Boylnae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00769; ERM; ]
                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and applications ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCB1_TAX10-9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145
                                                            54 QDYEE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Brain;
1 QUYEE 5
                                                                                                                                                                                                                EZRI_ HOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INIT MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                            P41976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIWAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
```

```
This SWISS PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss institute of Bioinformaties and the EMMH, outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Turunen (), Winqvist R., Pakkanen R., Grzeschik K. H., Wahlstroem T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Samelson L.E.; "Identilication of ezrin as an 81 kDa tyrosine phosphorylated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   !- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSAELETAL
STRUCTURES TO THE PLASMA MEMBRANE.
-!- SUBCELLULAR LOCATION: MICROVILLAR PERIPHERAL MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Egerton M., Moritz R.L., Druker B., Kelso A., Simpson R.J.; and indertification of the 70kD heat shock cognate protein (Hsc70) and alpha-actinin-1 as novel phosphotyrosine-containing proteins in Tlymphocytes.;
                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Frimates, Catarrhini, Hominidae, Homo.
NCBL_laxib-9006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- TISSUE SPECIFICITY: COMPONENT OF THE MICROVILLE OF INTESTINAL EPITHELIAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ottenwaelder B., Obermaier B., Mewes H.-W., Weil H., Wiemann S.; Submitted (MAR-2000) to the EMH,/GenBank/100BJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification of the two major epidermal growth factor-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tyrosine phosphorylation sites in the microvillar core protein ezrin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Egerton M., Burgess W.H., Chen D., Druker B.J., Bretscher A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cytovillin, a microvillar Mr 75,000 protein, chNA sequence, prokaryotic expression, and chromosomal localization.", J. Biol. Chem. 264:16727-16732(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gould K.L., Bretscher A., Esch F.S., Hunter T., and a control of the protein tyrosine kinase substrate, ezrin, reveals homology to band 4.1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -! - PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commus. 224:666-674(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
                                                              P153T1; P23714; 09NSJ4; 001-APR-1990 (Rel. 14, Created) (NNV-1990 (Rel. 120, Last Sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-90076135; Pubmed-2591371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7hem 267-19258-14265(1942).
                                                                                                                                                                                                                           Ezrin (p81) (Cytovillin) (Villin 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 171-179 AND 342-349.
MEDLINE-96311348; Pubmed-8713105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-89380299; PubMed-2674140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92406868; PubMcd-1382070;
Krieg J., Hunter T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92388649; PubMed-1381389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149:1847-1852(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBO J. 8:4133-4142(1989).
                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION BY PDGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CYTOPLASMIC SIDE).
                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immenel.
                                       EZRI_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaheri A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ...
∵
...
EZRI_HUMAN
```

0

Gaps

ć

0; Indels

0; Mismatches

Conservative

Best Local Similarity

Malches

1 ODYEE 5

Š

```
entities requires a license agreement (See http://www.isbrsib.ch/announce/arconnergialor send an email to license@isbrsib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright, it is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not tempored. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUNCTION: INVOLVED IN ANAPHASE SPINDLE ELONGATION.
SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY MYAK/KIF?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-96222363; FubMed-8636234, Well B. Foss M., Ready R., Cande W.Z.; Wein H., Foss M., Ready R., Cande W.Z.; "USK1, a novel kinesin-related profit from the distum Cylindrutheds fusiformis that is involved in anaphase spindle elongation."; J. Cell Biol. 133:595-604(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cylindrothera fusitormis (Marine diatom)
Eukaryota, stramenopiles, Bacillariophyta, Bacillariophyceae,
Hacillariophycidac, Bacillariates, Hacillariaces, Cylindrothero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 28; DB 1; Length 585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              indels
                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION (BY PDGFR). PHOSPHORYLATION (BY PUCKEY).
                                                                                                                                                                                                                                                                                                                                                                                                                                 2A844D140E3B06CC CRC54;
                                                                                                                                                                                                                                                                                        PROSITE, PSÓGGÓ, BAND_41_; 1.
PROSITE; PSO0661; BAND_41_2; 1.
PROSITE; PS50057; BAND_41_3; 1.
Structural procein; Cytoskeleton; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 35, Last sequence update)
(Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                  V -> L (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    624 AN
use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                       BAND 4.1-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              o a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred No.
                                                                                     EMBE; JOSO21; AAA61278.1; ALT_INIT.
EMRL: ALL62086; CAB92418.1: AET_INIT.
PIR: S09263: S09263.
PIR: A34400: A44400.
                                                                                                                                                                                                                  IPR000798; Ez/rad/moesin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ć
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                               InterPro; IPR000299; Band_4 1
                                                                                                                                                                                                                                                                                                                                                                                                                                 MW 29269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 0%;
                                                                                                                                                     P15311; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBI; U51680; AAB05681.1; -
HSSP; P17119; 3KAR.
                                                                                                                                                                                                                              Pfam; PF00373; Band_41; 1.
                                                                          EMBL: X51521; CAA35893.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Comservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDAPP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diatom spindle kinesin 1.
                                                                                                                                                                 Genew, HGNC.12691, VIL2
MIM; 123900; -
                                                                                                                                                                                                                                                            PRINTS; PROOF35; BAND41.
                                                                                                                                                                                                                                                                                                                                                                                                  353
                                                                                                                                                                                                                                                                           SMART; SM00295; B41; 1.
                                                                                                                                                                                                                                           Pfam; PF00769; ERM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               SAS AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N A
                                                                                                                                                                                                                                                                                                                                                                                  145
353
531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCB1_Tax1D-2853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel
                                                                                                                                                                                                                                                                                                                                                        57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 QDYEE 355
                                                                                                                                                     SWISS-2DPAGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QDYER 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSK1_CYLFU
                                                                                                                                                                                                                  InterPro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                     INIT MET
                                                                                                                                                                                                                                                                                                                                                                                    MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSK1_CYLFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
δλ
```

```
Mand Word V. Gwilliam P., Palandram M.A., Lyno M., Stewart A., RA Sqouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Ra Brooks K., Brown D., Brown S., Chilliangworth T., Charcher C.M., A Coulliss M., Connor R., Cronin A., Davis P., Fettwell T., Frascr A., Gotles S., Goble A., Hamlin N., Harris D., Hidalyo J., Hodgson G., RA Horroyd S., Hornby T., Howarth S., Muchell S., Magels K., Jones L., Jones M., Leather S., McDonald S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PWOT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diphosphate + 1-giutaminyl-tPNA(GIn).
-i- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 OCT 2001 (Ref. 40, East segmence update)
15 JUN-2002 (Ref. 41, Last annotation update)
Probable glutaminyl-tRNA synthetase (EC 6.1.1.18) (Glutamine--tRNA
                                                                                                                                                                                                                                                                                                                                                                                 .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   !- CAIALYING ACTIVITY: AIP + L-qlutamine + tRNA(Gln) = AMP +
                                                                                                                                                                                                                                                                                                                             190.0%; Score 28; 5B 1; Length 624;
                                                                                                                                                                                                         KINESIN-MOTOR (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                            DOSSEBPETLIBETSS CRO64;
                                                                                               PROSITE: PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE: PS50061; KINESIN_MOTOR_DOMAIN2: 1.
MOLOL PLOLEID, Microtubules, ATP binding, Colled Coll.
DOMAIN (FOTENTIAL).
                                                                                                                                                                                                                              COLLUED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota: Fungi: Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                     ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                       95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       811 AA.
                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPT;
InterPro, IFRG1772, kinesin_motor.
Piam: PFG0225, kinesin; 1.
Pkinis: PRG380; KinESINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDI.INE-21848401; PubMed-11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6-001-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                 70308 MW;
                                                                                                                                                                                                                                                                                                                                                       100.08;
                                                                                                                                                                                                                                                                                                                                                                              5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 415:8/1-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                      425
                                                                             SMART; SM00129: K1Sc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces.
                                                                                                                                                                                                                                                                               6.24 AM;
                                                                                                                                                                                                                                                                                                                                                       Host Logal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ligase) (GlnRS).
SPBC342.02.
                                                                                                                                                                                                                              425
186
                                                                                                                                                                                                    96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              505 QDYEE 509
                                                                                                                                                                                                                                                                                                                                                                                                                               1 QDYEE 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYQ_SCHPO
Q9Y7Y8;
                                                                                                                                                                                                                                                                                 SEVOENCE
                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                     NP BIND
                                                                                                                                                                                                         DOMA I N
                                                                                                                                                                                                                                NIAM
                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYQ_SCHPO
       6
```

```
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license isb sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DD20_HDMAN STANDARD; PRI; 824 AA.

O9UHIG: O94659: QSHIYO: QSHIXO: CSHIXO: CSHIXO: CSHIXO: CSHIXO: Last annotation update)

15 JUN-2002 (Rel: 41, Last annotation update)

16 JUN-2002 (Rel: 41, Last annotation update)

brobable ATP-dependent PNA helicase POX20 (DEAD-box profein DP 103) (Component of gems 3) (Gemin3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grundholf A.T., Kremmer E., Tureel O., Glieden A., Gindorf C., Atz J., Mueller-Gantzsch N., Schubach W.H., Grasser F.A., "Characterization of DP103, a novel DPAD box protein that binds to the Epstein-Harr virus nuclear proteins EMNA2 and EHNA3C.";
J. Biol. Chem. 274:19136-19144(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRINTS; PROUME; taxing trighted alus; 1.
TIGREAMS; TIGRO0440; alus; 1.
FROSTITE; PROUTE; AA_IRNA_LIGASE_I; 1.
Amitoacy: triand synthetas; Protein biosynthesis; Ligase, AiP-binding.
SITE 269 279 "HIGH" RIGION.
SITE 502 506 "KMSKE" REGION.
BINDING 505 505 ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genins: a novel DEAD bex protein that interacts with SMN, the spinal muscular atrophy gene product, and a component of genes.";
J. Cell Hiol. 147:1181-1194(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND MASS SPECIROMETRY.
MEDLINE-20069784; Pubmed-10601333;
Charroux B., Pellizzoni I., Perkinson P.A., Sheychenko A., Mann M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isoqai T., ota T., Hayashi K., Suqiyama T., Otonki T., Suluki Y., Nishikawa T., Nadai K., Sugano S., Ishikashi T., Fujimori K., Tanai H., Kimata M., Watanabo M., Hisaoka S., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 28; DB 1; Length 811;
100.0%; Pred. No. 1.3e+02;
.ive 0; Mismatches 0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        la; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Masuho Y., Kanchori K.;
"NEDo human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP 1999) to the PMRE/Cornank/DORT databases
                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPRG00924; Glu_FRNA-synt_lc.
InterPro; IPRG01412; tRNA-synt_l.
Plam; PF00749; tRNA-synt_lc; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-99315855; PubMed-10383418;
                                                                                                                                                                                                                                                                      EMBL; AL096809; CAB46772.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hest Local Similarity 100.0
Matches 5: Conservative
                                                                                                                                                                                                                                                                                                                                                    InterPro, IPRO04514; Glus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                    1GTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                    P00962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QDYEE 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 ODYRES 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dreyluss G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE STANFORM TO STANFAR THE ST
```

```
between the Swiss Institute of Bioinformalies and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way monofiled and this statement is not removed. Usage by and for commercial entities replies a license above. (See ETTE (Www.st.st.ch.) or send an email to license sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                  Ansorge W., Wirkner U., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (DEC-1999) to the EMBL/GenHank/DBLJ databases.
-!- FUNCTION: HE SMN COMPLEX PLAYS AN ESSENITAL KOLE IN SPLICEOSOMAL.
SNRNP ASSEMBLY IN THE CYTOPLASM, AND IS REQUIRED FOR FRE-MKNA
SPLICING IN THE NUCLEUS.
-! SUBGNIT: FERMS A STABLE HETEROMERIC COMPLEX WITH SURVIVAL OF MOTOR
                                                                                                                                                                                                                                                                                                                                                                             NEURON PROFEIN (SMN), GEMINZ AND GEMINA. INTERACTES DIRECTLY WITH SAN, SM P, SM D2 AND SM D3. INTERACTS WITH ERVERAZES AND ENNAGE SUBCELLULAR LOCALIZED IN SUBCELLULAR LOCALIZED TO COLLED BEDIES, CALLED GEMS, WHICH SKEDNOCLEAR STRUCTURES NEXT TO COLLED BEDIES, CALLED GEMS, WHICH ARE HIGHLY ENROCHED IN SPLICESOMAL SURNPS.

SIMILARITY: BELONGS TO THE DEAD HOX HELLCASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
Helicase; ATF-Lindina, DNA-bindina, Nuclear protein, mRNA processing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F\to V (1N REF. 2). 
 Y\to C (1N REF. 4). 
 YMHRIGRAGRF -- MIYYLTESILL (1N REF. 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I > T (IN REF. 5 AND 6).
R -> K (IN REF. 1).
Y -> H (IN REF. 1).
G -> S (IN REF. 1).
S -> T (IN REF. 1).
S -> T (IN REF. 1).
W; 76712F034B2A00F2 GR064;
                                                                                                       Submitted (JUL 2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 28; DB ]; 1. 100.0%; Pred. Nc. 1.3c.02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMN_INTERACTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000629; DEAD_box.
InterPro; IPR001650; Helicase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF171063; AAF14544.1; -. EMBL; AF106019; AAD42744.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AL049557; CAB55686.2; -: EMBL, AR001796; BA93727.1; -: EMBL, AR017556; ARB11556.1; -: EMBL, AL133598; CAB63734.1; -: EMBL, AL135598; CAB63734.1; -: EMBL, AL13598; CAB63734.1; -: EMBL, AL135598; CAB63734.1; -: EMBL, AL135598; -: EMBL, AL1355988; -: EMBL, AL135598; -: EMBL, AL135598; -: EMBL, AL135598; -: E
                                                                                                                                                              SEQUENCE OF 393-824 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ptam; PF00271; helicase_C; 1.
SMART; SM00487; DEXDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92240 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro: IPR001410; DEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                local Similarity 100.
Les 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGNC: 2743; DDX20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM00490; HEILICG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279
403
646
639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  659
676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00270; DEAD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113
214
548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1111/8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  824 AA;
                         SEQUENCE FROM N.A.
                                                TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    393
636
639
659
676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106
                                                                                   Strausberg R.;
                                                                                                                                                                                           TISSUE-Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; Q58083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ODYEE 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 606168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spliceosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMA I N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
```

771 ODYEE 775

RESULT 11 DD20_MOUSE 772 ODYEE 776

1 QDYEE 5

```
between the Swiss institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                       Davies K.E.;
"Direct interaction of Smn with dpl03, a putative RNA helicase: a role for Smn in transcription regulation?";
Hum. Mol. Genet 9:1094-1100(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPLICING IN THE NUCLEUS.
SUBUNITY FORMS A SIGNOR HETER MERIT OF MPLEX MITH SURVIVAL OF MOTOR NEURON PROTEIN (SMN), GEMINZ AND GEMINZ AND GEMINZ AND GEMINZ AND SM B, SM D, AND SM D3.
                                                                   16-0CT-2001 (Ref. 40, Last annotation update)
Probable ATP-dependent PNA helicase DDX20 (DEAD-box protein 20) (DEAD-box protein DP 103) (Component of gems 3) (Gemins) (Regulator of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-2000) to the PMRI/AppRank /PDH1 darabases
-!- FUNCTION: THE SMN COMPLEX PLAYS AN ESSENTIAL ROLE IN SPLICEOSOMAL.
SNRNP ASSEMBLY IN THE CYTOPLASM, AND IS PEQUIPED FOR PRE-MPNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicase, ATP-binding, DNA-binding, Narlear protein; mPNA provessing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLUIAR LOCATION: CYTOPLASMIC AND NUCLEAR, LOCALIZED IN SUBNUCLEAR STRUCTURES NEXT TO COLLED MODIES, CALLED GEMS, WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                       on Q = Modifier T F, Ford C , YDC XL, Crawford F A , Sadorsky T .
"The DEAD box protein DP10% is a regulator of steroidogenic factor-
                                                                                                                                                                                     Rukaryota, Metazoa, Chordata, Chamiata, Vertebrata; Enteleostomi,
Mammalia: Eutheria, Rodenlia, Spinjognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                       Campbell L., Hunter K.M., Mohaghegh P., Tinsley J.M., Brasch M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 28, DB 1; Length 825, 160.0%; Pred: No. 1.3e/52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARE HIGHLY ENRICHED IN SPLICEOSOMAL SNRNPS.
SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 A -> T (IN REF. 2).

9 P -> R (IN REF. 2).

10 P -> R (IN REF. 2).

11 P -> T (IN REF. 2).

12 P -> T (IN REF. 2).

13 P -> T (IN PEF. 2).

14 P -> T (IN PEF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATF (POTENTIAL).
           093784; 093784;
16-00T-2001 (Rel. 40, Created)
16-00T-2001 (Rel. 40, Last Scylence update)
 825 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSILE: PS00039; DEAD_ATP_HELICASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEAD BOX.
 PRT;
                                                                                                                                                                                                                                                                               MEDLINE-20231537; PubMcd-10757334;
                                                                                                                             steroidogenic factor-1) (ROSF-1).
DDX20 OR GEMIN3 OR DP103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro: IPROGO629; DFAD_box.
InterPro: IPROG1650; Helicase_C.
Plam; PF00270; DEAD; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ250027; CAB86201.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BALB/c; TISSUE-Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF220454; AAF76301.1; ... Q58083; 1HV8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00271; helicase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1858415; Ddx20.
InterPro; 1PR001410; DEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00487; DEXDC; 1.
SM00490; HELLCC; 1
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114
215
                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 825 AA;
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spliceosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFILICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plam;
CHHILLERMESS CSCREEE ERED E COCCCCCCE E COCCCCE E CERT E COCCCC E COCCCE E COCCC E COCCC E COCCC E COCCC E COCC
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the LMBs outstation the Lutypean Bicinformatics Institute. There are no Testrictions on Its use by non-profit institutions as last once it is no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARDIOVASCULAR INSTABILLTY, RECURRENT PNEUMONIAS, VOMÍTING CRISES, MON GASÍFICANIESTINAL DYSFUNCILLON. 11 IS PERMARLLY CONFINED TO INDIVIDIALS OF ASFRENAZI JEMISH DESCENI, WITH AN INCIDENCE OF 1/4600 110F REPURS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISEASE: DEFECTS IN IXBRAP ARE THE CAUSE OF FAMILIAL DYSAUTONOMIA CED; ALEX NOWN AS RILEY-DAY SYNDROME ON HERELITAKY SENSORY AND AUTONOMIC NEUROSATHY TYPE III. THIS AUTOSOMAL RECESSIVE DISORDER IS DUE TO THE POOR DEVELOPMENT AND SURVIVAL, AND PROGRESSIVE DECENERATION OF THE SENSORY, SYMMATHETIC AND PARASYMPATHETIC NEUROWS ET INDIVIDUALS APE AFFECTED WITH A VARIETY OF SYMPTOMS SUCH AS DECHEBASED SENSITIVITY TO PAIN AND TEMPERATURE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scheidereit C., Maayan C., Axeirod F.B., Gusella J.F.; "Tissue specific expression of a splicing mutation in the IKBKAP gene causes familial dysautonomia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-210-00-44. PubMed-11210-921.

MEDLINE-210-00-44. PubMed-11210-921.

MEDLINE-210-00-44. PubMed-11210-921.

Model S.A., Ekstein J., Rubin B.Y.:

Polipi S.A., Ekstein J., Rubin B.Y.:

Polipi S.A., Ekstein J., Rubin B.Y.:

Man I Hum Genet KB.75-75-758 (2001).

Man T Hum Genet KB.75-75-758 (2001).

MAN ACT AS A SCAFFOLD PROTEIN THAT MAY ASSEMBLE ACTIVE IK-HWITION: MAY ACT AS A SCAFFOLD PROTEIN THAT MAY ASSEMBLE ACTIVE IK-MAPSA14 COMPLEXES (IKRA, IKKB AND MAFSK14/NIK).

MEN-ALPHA AND IK-HETA.

MEN-ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFGSENCE FPCM N.A., AND VARIANT FD PRO-696.
MEDLINE-21090531: Pubmed-1179008.
Slangenbarpt S.A., Blumenteld A., Gill S.P., Leyne M., Muil J.,
Slangenbarpt S.A., Liebert C.B., Chadwick B.P., Idelson M., Reznik L.,
Robbins C.M., Makalowska I., Brownstein M.J., Krappmann D.,
                                                                                                                                  095163; UMB27; Q9UGB7;
16-OCT-2001 (Rel 40, Created)
10-OCT-2001 (Rel 40, Last ascounce update)
26-OCT-2001 (Rel 40, Last annolation update)
1RappaB kinase complex-associated protein (IKK complex-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Fukaryota: Metazga: Chordata: Craniata; Vertebrata; Luteleostomi;
Mammalia: Butheria: Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Heather B., Mewes H. W., Gassenhuber J., Wiemann S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAUTION: REE. 3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A PRAMESHIFT IN POSITION 1286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cohen L., Henzel W.J., Baeuerle P.A.; "IRAF is a scarfold protein of the Ikappab kinabe complex."; Nature 395:292-296(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT ED PRO-696, AND EFFECT ON PHOSPHORYLATION.
                                                                                                        PRT; 1332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE PROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Hum. Genet. 68:598-605(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Cervical carcinoma;
MEDLINE-98421679; PubMed-9751059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE OF 961-1332 FROM N.A.
                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                            protein) (p150).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     IKHKAP OR IKAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Brain;
                                                                                                  I KAP_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wambutt R
RESULT 12
IKAP_HUMAN
                                                                                                                                                                                                                                               TERROSOS SERVINA E A MARKA MAR
```

ć

Sdes

ċ

Indels

O; Mismatches

5; Conservative

Best Logal Similarity

Matches

```
This SWISS-PROT entry is copyright. It is produced through a collaboration the way as institute of Brioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed "many by and for commercial entities requires a license afterement (See http://www.isb-sib.ch/announcc/or send an email to license-lisb sib.eh).
entities requires a license agreement (See http://www.isb-sib.ch/annonnee/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .:
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIJURE-96437999; PubMed-8688087; Mou L., Fleischmann R.D., Marin C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Accayne J.D., Suffon G.G., Hake I.A. Eirrorald I.M., Clayten P.A., Geograph J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich G.I., Overfleek R. K., Kirkness E.F., Weinstock K.G., Merrick A.M., Glodek A., Scott J.L., Geoghauen N.S. W. Weidman T.F., Pukmann T.L., Nguyen F. Offerback I.R., Kelley J.M., Feterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Koberts K.M., Hurst M.A., Kaine B.P., Hordodowsky M., Klenk H.-P., Fraser C.M., Smith H.-G., Woose C.R., Venter J.C., "Complete genome Sequence of the methanovenic archaeon, Methanosurcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 28; DB 1; Length 1332; US.08; Fred. Mc. 2.2c+02; Ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                     -> P (IN FD; MILD PHENOTYPE;
                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION IS REDUCED).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea; Euryarchaeota; Methanococci; Methanococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 58 GLU-RICH.
82 AA: 9507 MW: 298230477H2C550B CPC64;
                                                                                                                                                                                                                                                                                                                                                              /F11d-VAR_011327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NnV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJ0070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methanoraldocoreaceae; Methanoraldococeus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Complete profeome.
                            or send an email to licensedish sib, ch).
                                                                                                                EMBL; AF154419; AA343369.1; -.
EMBL; AL049945; CAB43219.1; ALL_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
                                                                                                                                                                                                                                                                   Phosphorylation, Disease mutation.
VARIANT 696 696 R - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Ref. 35, Created)
                                                                                       EMBL; AF044195; AAC64258.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 273:1058 1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U67464; AAB98053.1; -
                                                                                                                                                                           Genew, HONC:5959; IKBKAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              961
1072
1158
1320
                                                                                                                                                                                                                                                                                                                                                                                                                   312 31
754 75
961 96
1072 107
1158 115
1320 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         wat Similarity
s 5: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N'B1_TaxID-2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1074 QDYEE 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGR: MJ0070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ODYEE 5
                                                                                                                                                                                                        MIM; 603722;
                                                                                                                                                                                                                                          MIM; 223900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y070_METJA
ID Y070_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        060373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE WAS COUNTRIED TO A SERVICE OF COUNTRIES OF A SERVICE OF COUNTRIES OF A SERVICE OF COUNTRIES OF COUNTRIES
                                                        ŝ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation her Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.sih.ch/annonnee/
                                                                                                                                                                                                                                                                                                                                                                                                                                               alpha and beta genes.";
DNA Seq. 12:131-135(2001).
-!- FUNCTION: CGRP induces vasodilatation. It dilutes a variety of vessels including the coronary, cerebral and systemic vasculature. Its abundance in the CNS also points toward a neurotransmitter or neuromodulator role (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMIDATION (G 121 PROVIDE AMIDE GROUP) (BY
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-129/Sv;
MEDLINE-15064265, FubMed 11761712;
Thomas P.M., Masonkin I., Zhang H., Gaqel R.F., Cole G.J.;
"Structure of the mouse calcitonin/calcitonin gene-related peptide
                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Greated)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Calcitonin gene-related peptide II precursor (CGRP II) (Heta-type
                                                                                                                                                                                                                                                                                                          Eukaryota; Melazoa; Chordata; Craniata: Vertebrata; Euteleostomi;
Mammalia; Eutheria: Pedentia; Sciurequathi: Muridae; Musinae; Mus
                                  .;
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
CALCITONIN GENE-RELATED PEPTIDE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cleavage on pair of basic residues; Amidation; Hormone; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.3%; Score 25; DB 1; Length 130;
DB 1; Length 82;
                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97299244E8F6C536 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
                                1; Mismatches
              Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to licensewisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY)
 Score 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR001693; Calcitonin like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF325524; AAK16431.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002163; Calcitonin_B. Pfam; PF00214; Calc_CGRP_IAPP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMARI; SMOÖLLS; CALCITONIN; 1.
PPOSITE; PSOO258; CALCITONIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0818; ISLETAMYLOID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14623 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS: PRO0817; CALCITONINH.
84.48;
                80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000443; Amylin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF325526; AAK16431.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.08;
                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCALION:
                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Calcb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
130
50
120
                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 AA;
                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                         SHOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            NCBI_LIGXID 10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:2151254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27
84
127
85
                                                                                         51 EDYEE 55
                                                           1 ODYRE 5
                                                                                                                                                                   CAL2_MOUSE
Q99MP3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROPEP
DISULFID
Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROPER
                                                                                                                                                                                                                                                            CGRP).
                                                                                                                                        RESULT 14
CAL2_MOUSE
                                                                                                                                                                                                                                                                                CALCE
                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best
                                                             ò
```

1 ODYEE 5

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Rioinformatics and the EMBL outstation. The European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as iong as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb.sib.ch/announce/or send an email to licensedisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homologous to calcinonin gene-related peptide.";
Science 229:1094-1097(1985).
--- Function. GGP induces vasciflatation. It dilates a variety of
vessels including the coronary, cerebral and systemic vasculature.
Its abundance in the CNS also points toward a neurotransmitter or
neuromodulator role.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
AMIDATION (G-126 PROVIDE AMIDE GROUP) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Expression in brain of a messenger RNA encoding a movel neuropeptide
                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Kat).
Eukaryota, Metazca; Chordata; Cramiata; Vertebrata, Butelcostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sidbo
                                                                                                                                                                                                                                                                                                            Calcitonin gene-related peptide II precursor (CGRP-II) (Beta-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002163; Calcitonin_B.
Pfam; PF00214; Calc_CGRP_IAPP; T.
PRINTS: PR00817; CALGITONINB.
SMART: SMO0113; CALCITONIN. 1.
PRUSITE; PS00258; CALCITONIN. 1.
Cleavage on pair of basic residues; Amidation; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
CALCITONIN GENE-RELATED PEPTIDE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amara S.G., Arriza J.L., Leff S.E., Swanson L.W., Evans R.M.,
Rosenfeld M.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.3%; Score 25; DB 1; Length 134; 80.0%; Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HF6CAFB87A489B38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -! - SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
                                                                                                                                                                                 P10093;
01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                           134 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001693; Calcitonin-like.
                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE-85300490; PubMed-2994212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 AA: 14965 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M11596; AAA40850.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26
86
125
134
95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A44173; A44173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCB1_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27
89
131
90
125
56 QDYEQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 QDYEQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QUYRE 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - <del>- 7</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                           CAL2_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEPIIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                             KESU1.1 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                       CAL2_RAT
                                                                                                                                                           NOTE THE TEXT OF THE PROPERTY OF THE PARTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PARTY OF TH
```

Search completed: January 16, 2,003, 16:51:17 Job time : 8,28571 sees

			:	
	• •	•	,	